

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: Human_BVR 296 aa
Sequence 2: Rat_BVR 295 aa
Sequence 3: Mouse_BVR 295 aa
Sequence 4: Pig_BVR 296 aa

Start of Pairwise alignments Aligning...

Sequences (1:2) Aligned. Score: 82
Sequences (1:3) Aligned. Score: 81
Sequences (1:4) Aligned. Score: 98
Sequences (2:3) Aligned. Score: 88
Sequences (2:4) Aligned. Score: 83
Sequences (3:4) Aligned. Score: 82

Start of Multiple Alignment

There are 3 groups Aligning...

Group 1: Sequences: 2 Score:6353
Group 2: Sequences: 2 Score:6075
Group 3: Sequences: 4 Score:5825
Alignment Score 9407

CLUSTAL W (1.82) multiple sequence alignment

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Human_BVR  MNAEPRKFGVVVVGVGRAGSVRMRDLRNPSPSAFLNLIGFVSRRELGSIDGVQQISLE 60
Pig_BVR    MNAEPRKFGVVVVGVGRAGSVRMRDLRNPSPSAFLNLIGFVSRRELGSIDGVQQISLE 60
Rat_BVR    MDAEPRKRFVGVVVGVGRAGSVRLRDLKDPR-SAAFLNLIGFVSRRELGSLDEVQRISLE 59
Mouse_BVR  MSTEPKRKFGVVVVGVGRAGSVRIRDSKDPH-SSAFLNLIGYVSRRELGSLDNVRQISLE 59
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Human_BVR  DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLEYPMTLSLAAAQELWELAEQKGKV 120
Pig_BVR    DALSSQEVEVAYICSESSSHEDYIRQFLNAGKHVLEYPMTLSLAAAQELWELAEQKGKV 120
Rat_BVR    DALRSQEIDVAYICSESSSHEDYIRQFLQAGKHVLEYPMTLSFAAAQELWELAAQKGRV 119
Mouse_BVR  DALRSQEVDAVAYICTESSSHEDYIRQFLQAGKHVLEYPMALSFAAAQELWELAAQKGRV 119
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Human_BVR  LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFSTDPLEEDRFGFPAFSGISRLTWLVSLF 180
Pig_BVR    LHEEHVELLMEEFAFLKKEVVGKDLLKGSLLFSTAGPLEEERFGSPAFSGISRLTWLVSLF 180
Rat_BVR    LHEEHVELLMEEFEFLRREVLGKELLKGSRLFTASPLEEERFGFPAFSGISRLTWLVSLF 179
Mouse_BVR  LHEEHIELLMEEFEFLKREVAGKELLKGSRLFTASPLEEEKFGFPAFSGISRLTWLVSLF 179
*****:***** **.:** **.:***** **.:*****:*** *****:*****

Human_BVR  GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240
Pig_BVR    GELSLVSATLEERKEDQYMKMTVCLETEKKSPLSWIEEKGPGLKRNRYLSFHFKSGSLEN 240
Rat_BVR    GELSLISATLEERKEDQYMKMTVQLETQNKGLLSWIEEKGPGLKRNRYVNFQFTSGSLEE 239
Mouse_BVR  GELSLISATMENRKEDQYMKMTVQLETQNKSPLSWIEEKGPGLKRNRIHSIHFKSGSLEE 239
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Human_BVR  VPNVGVNKNIFLKDQNIQVQKLLGQFSEKELAAEKKRILHCLGLAEIQQYCCSRK 296
Pig_BVR    VPNVGVNKNIFLKDQNIQVQKLLGQFSEKELAAEKKRILHCLGLAEIQQYCCSRK 296
Rat_BVR    VPSVGVNKNIFLKDQDIQVQKLLQVSAEDLAAEKKRIMHCLGLASDIQKLCHQKK 295
Mouse_BVR  VPNVGVNKNIFLKDQDIQVQKLLGQVSAEDLAAEKKRILHCLGLASDIQRLCHRKQ 295
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